Resource Summary Report

Generated by dkNET on Apr 29, 2025

LDHAT

RRID:SCR_006298
Type: Tool

Proper Citation

LDHAT (RRID:SCR_006298)

Resource Information

URL: http://www.stats.ox.ac.uk/~mcvean/LDhat/

Proper Citation: LDHAT (RRID:SCR_006298)

Description: Software package for the analysis of recombination rates from population genetic data (entry from Genetic Analysis Software)

Abbreviations: LDHAT

Resource Type: software resource, software application

Keywords: gene, genetic, genomic, c, dos

Funding:

Resource Name: LDHAT

Resource ID: SCR_006298

Alternate IDs: nlx_154423

Record Creation Time: 20220129T080235+0000

Record Last Update: 20250429T055043+0000

Ratings and Alerts

No rating or validation information has been found for LDHAT.

No alerts have been found for LDHAT.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 44 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Ferguson S, et al. (2024) Exploring the role of polymorphic interspecies structural variants in reproductive isolation and adaptive divergence in Eucalyptus. GigaScience, 13.

Dinh BL, et al. (2024) Recombination map tailored to Native Hawaiians may improve robustness of genomic scans for positive selection. Human genetics, 143(1), 85.

Akther S, et al. (2024) Natural selection and recombination at host-interacting lipoprotein loci drive genome diversification of Lyme disease and related bacteria. mBio, 15(9), e0174924.

Dinh BL, et al. (2023) Recombination map tailored to Native Hawaiians improves robustness of genomic scans for positive selection. bioRxiv : the preprint server for biology.

Krishnan S, et al. (2023) Rhometa: Population recombination rate estimation from metagenomic read datasets. PLoS genetics, 19(3), e1010683.

Epstein R, et al. (2023) Exploring impact of recombination landscapes on breeding outcomes. Proceedings of the National Academy of Sciences of the United States of America, 120(14), e2205785119.

Versoza CJ, et al. (2022) The recombination landscapes of spiny lizards (genus Sceloporus). G3 (Bethesda, Md.), 12(2).

Wertheim JO, et al. (2022) Detection of SARS-CoV-2 intra-host recombination during superinfection with Alpha and Epsilon variants in New York City. Nature communications, 13(1), 3645.

Wang L, et al. (2022) Linked selection, differential introgression and recombination rate variation promote heterogeneous divergence in a pair of yellow croakers. Molecular ecology, 31(22), 5729.

Lynch M, et al. (2022) The Linkage-Disequilibrium and Recombinational Landscape in Daphnia pulex. Genome biology and evolution, 14(11).

Liu S, et al. (2022) Demographic History and Natural Selection Shape Patterns of Deleterious Mutation Load and Barriers to Introgression across Populus Genome. Molecular biology and evolution, 39(2).

Schreiber M, et al. (2022) Recombination landscape divergence between populations is

marked by larger low-recombining regions in domesticated rye. Molecular biology and evolution, 39(6).

Fuentes RR, et al. (2022) Domestication Shapes Recombination Patterns in Tomato. Molecular biology and evolution, 39(1).

Ye Z, et al. (2022) Genetic Diversity, Heteroplasmy, and Recombination in Mitochondrial Genomes of Daphnia pulex, Daphnia pulicaria, and Daphnia obtusa. Molecular biology and evolution, 39(4).

do Socorro Fôro Ramos E, et al. (2021) High Heterogeneity of Echoviruses in Brazilian Children with Acute Gastroenteritis. Viruses, 13(4).

Patiño-Galindo JÁ, et al. (2021) Global Patterns of Recombination across Human Viruses. Molecular biology and evolution, 38(6), 2520.

Hassan S, et al. (2021) High-resolution population-specific recombination rates and their effect on phasing and genotype imputation. European journal of human genetics : EJHG, 29(4), 615.

Zanardo LG, et al. (2021) Experimental evolution of cowpea mild mottle virus reveals recombination-driven reduction in virulence accompanied by increases in diversity and viral fitness. Virus research, 303, 198389.

Stauber L, et al. (2021) Emergence and diversification of a highly invasive chestnut pathogen lineage across southeastern Europe. eLife, 10.

Moran RL, et al. (2020) Genomic Resources for Darters (Percidae: Etheostominae) Provide Insight into Postzygotic Barriers Implicated in Speciation. Molecular biology and evolution, 37(3), 711.